

## SEQUENCE LISTING

<110> Universite Liege

<120> Hybrid proteins of active-site serine  $\beta$ -lactamase

<130> 2002-24

<140>

<141>

<150> EP 04 075 430.1

<151> 2004-02-11

<160> 41

<170> PatentIn Ver. 2.1

<210> 1

<211> 858

<212> DNA

<213> Escherichia coli

<220>

<223>  $\beta$ -lactamase TEM-1 gene (complementary strand)

<400> 1

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tgctgcaatg ataccgcgag acccacgctc accggtcca gatttatcag caataaacca 180
gccagccgga agggccgagc gcagaagtgg tcttgcaact ttatccgcct ccatccagtc 240
tattaattgt tgccgggaag ctagagtaag tagttcgcca gttaatagtt tgcgcaacgt 300
tgttgccatt gctgcaggca tcgtgggtgc acgctcgtcg tttgggtatgg cttcattcag 360
ctccggttcc caacgatcaa ggcgagttac atgatcccc atggttggtgca aaaaagcggg 420
tagctccttc ggtcctccga tcgttggtcag aagtaagttg gccgcagtgt tatcactcat 480
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gactgggtgag tactcaacca agtcattctg agaatagtgt atgcggcgac cgagttgctc 600
ttgcccggcg tcaacacggg ataataccgc gccacatagc agaactttaa aagtgtcat 660
cattgaaaaa cgttcttcgg ggcgaaaact ctcaaggatc ttaccgctgt tgagatccag 720
ttcgatgtaa cccactcgtg caccacaactg atcttcagca tcttttactt tcaccagcgt 780
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gaaatgttga atactcat                                     858
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<210> 2

<211> 921

<212> DNA

<213> Bacillus licheniformis

<220>

<223>  $\beta$ -lactamase BlaP gene

<400> 2

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atgaaattat ggttcagtag tttaaaactg aaaaaggctg cagcagtggt gcttttctct 60
tgcgtcgcgc ttgcaggatg cgctaacaat caaacgaatg cctcgcaacc tgccgagaag 120
aatgaaaaaga cggagatgaa agatgatttt gcaaaacttg aggaacaatt tgatgcaaaa 180
ctcgggatct ttgcattgga tacaggtaga aaccggacgg tagcgtatcg gccggatgag 240
cgttttgctt ttgcttcgac gattaaggct ttaactgtag gcgtgctttt gcaacagaaa 300
tcaatagaag atctgaacca gagaataaca tatacacgtg atgatcttgt aaactacaac 360
ccgattacgg aaaagcacgt tgatacggga atgacgctca aagagcttgc ggatgcttcg 420
cttcgatata gtgacaatgc ggcacagaat ctattctta aacaaattgg cggacctgaa 480
agtttgaaaa aggaactgag gaagattggg gatgagggtta caaatcccga acgattcgaa 540
ccagagttaa atgaagtga tccgggtgaa actcaggata ccagtacagc aagagcactt 600
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gtcacaaagcc ttcgagcctt tgctcttgaa gataaaacttc caagtgaataa acgcgagctt 660
ttaatcgatt ggatgaaacg aaataccact ggagacgcct taatccgtgc cgggtgtgccg 720
gacgggttggg aagtggctga taaaactgga gcggcatcat atggaaccgc gaatgacatt 780
gccatcattt ggccgcaaaa aggagatcct gtcgttcttg cagtattatc cagcagggat 840
aaaaaggacg ccaagtatga tgataaactt attgcagagg caacaaagggt ggtaatgaaa 900
gccttaaaca tgaacggcaa a                                     921

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&lt;210&gt; 3

&lt;211&gt; 975

&lt;212&gt; DNA

<213> *Streptomyces cacaoi*

&lt;220&gt;

<223>  $\beta$ -lactamase BlaL gene

&lt;400&gt; 3

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atgcgtatcc gtcccacccg tcgtcttctc ctcggcgcgg tcgcgcgcgt cgccctcggt 60
ccgctggtgg cctgcggtca ggcgtcgggc tccgagagcg gccagcagcc cggcctcggc 120
ggttgcggga cgagcgaca cggtcgcggc gacgcccacg agaaggagtt ccgggcgctg 180
gagaagaagt tcgacgcca ccctggcgtc tacgccatcg acaccgcga cggccaggag 240
atcacccacc gggccgacga gcgcttcgcc tacggctcga ccttcaaggc cctccaggcg 300
ggcgcgatcc ttgcgcaagt tctccgagac gggcgcgaa tccggcgggg cgccgaggcc 360
gacggcatgg acaaggtggt ccactacggg caggacgcga tcctgcccac ctcaccggtg 420
accgagaagc acgtcgcgga cggcatgtcc ctgcgcgagc tgtgcgacgc cgtcgtggcc 480
tacagcgaca acaccgcggc caacctgctc ttcgaccagc tcggcgggcc aaggggctca 540
acgcgggtcc tcaagcagct cggcgaccac accacgagca tggaccgcta cgagcaggag 600
ctgggctcgg ccgtcccccg cgaccccccg gacaccagca cgccgcgcgc gttcgccgag 660
gacctgcgcg ccttcgcgtg cgaggacggc gagaaggccg ccctcgcgcc caacgaccgc 720
gagcagctga acgactgcat gagcgggagc aggaccggcg acgcgctgat ccgggcccgt 780
gtgccgaagg actggaagg ggaggacaag agcggccagg tcaagtacgg caccgggaac 840
gacatcgccg tcgtccgccc gcccggccgc gcgccgatcg tcgtctcggt gatgagccac 900
ggcgacaccc aggacgccga gccgcacgac gagctggtgg ccgaggccgg cctcgtcgtc 960
gccgacggtc tgaag                                     975

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&lt;210&gt; 4

&lt;211&gt; 286

&lt;212&gt; PRT

<213> *Escherichia coli*

&lt;220&gt;

<223>  $\beta$ -lactamase TEM-1

&lt;400&gt; 4

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Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
 1             5             10             15

Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
      20             25             30

Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
      35             40             45

Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
      50             55             60

Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
      65             70             75             80

Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
      85             90             95

```

## 3.

Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr  
 100 105 110

Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser  
 115 120 125

Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys  
 130 135 140

Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu  
 145 150 155 160

Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg  
 165 170 175

Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu  
 180 185 190

Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp  
 195 200 205

Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro  
 210 215 220

Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser  
 225 230 235 240

Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile  
 245 250 255

Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn  
 260 265 270

Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp  
 275 280 285

&lt;210&gt; 5

&lt;211&gt; 307

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;220&gt;

<223>  $\beta$ -lactamase BlaP

&lt;400&gt; 5

Met Lys Leu Trp Phe Ser Thr Leu Lys Leu Lys Lys Ala Ala Ala Val  
 1 5 10 15

Leu Leu Phe Ser Cys Val Ala Leu Ala Gly Cys Ala Asn Asn Gln Thr  
 20 25 30

Asn Ala Ser Gln Pro Ala Glu Lys Asn Glu Lys Thr Glu Met Lys Asp  
 35 40 45

Asp Phe Ala Lys Leu Glu Glu Gln Phe Asp Ala Lys Leu Gly Ile Phe  
 50 55 60

Ala Leu Asp Thr Gly Thr Asn Arg Thr Val Ala Tyr Arg Pro Asp Glu  
 65 70 75 80

Arg Phe Ala Phe Ala Ser Thr Ile Lys Ala Leu Thr Val Gly Val Leu  
 85 90 95

Leu Gln Gln Lys Ser Ile Glu Asp Leu Asn Gln Arg Ile Thr Tyr Thr  
 100 105 110  
 Arg Asp Asp Leu Val Asn Tyr Asn Pro Ile Thr Glu Lys His Val Asp  
 115 120 125  
 Thr Gly Met Thr Leu Lys Glu Leu Ala Asp Ala Ser Leu Arg Tyr Ser  
 130 135 140  
 Asp Asn Ala Ala Gln Asn Leu Ile Leu Lys Gln Ile Gly Gly Pro Glu  
 145 150 155 160  
 Ser Leu Lys Lys Glu Leu Arg Lys Ile Gly Asp Glu Val Thr Asn Pro  
 165 170 175  
 Glu Arg Phe Glu Pro Glu Leu Asn Glu Val Asn Pro Gly Glu Thr Gln  
 180 185 190  
 Asp Thr Ser Thr Ala Arg Ala Leu Val Thr Ser Leu Arg Ala Phe Ala  
 195 200 205  
 Leu Glu Asp Lys Leu Pro Ser Glu Lys Arg Glu Leu Leu Ile Asp Trp  
 210 215 220  
 Met Lys Arg Asn Thr Thr Gly Asp Ala Leu Ile Arg Ala Gly Val Pro  
 225 230 235 240  
 Asp Gly Trp Glu Val Ala Asp Lys Thr Gly Ala Ala Ser Tyr Gly Thr  
 245 250 255  
 Arg Asn Asp Ile Ala Ile Ile Trp Pro Pro Lys Gly Asp Pro Val Val  
 260 265 270  
 Leu Ala Val Leu Ser Ser Arg Asp Lys Lys Asp Ala Lys Tyr Asp Asp  
 275 280 285  
 Lys Leu Ile Ala Glu Ala Thr Lys Val Val Met Lys Ala Leu Asn Met  
 290 295 300  
 Asn Gly Lys  
 305

<210> 6  
 <211> 325  
 <212> PRT  
 <213> Streptomyces cacaoi

<220>  
 <223>  $\beta$ -lactamase BlaL

<400> 6  
 Met Arg Ile Arg Pro Thr Arg Arg Leu Leu Leu Gly Ala Val Ala Pro  
 1 5 10 15  
 Leu Ala Leu Val Pro Leu Val Ala Cys Gly Gln Ala Ser Gly Ser Glu  
 20 25 30  
 Ser Gly Gln Gln Pro Gly Leu Gly Gly Cys Gly Thr Ser Ala His Gly  
 35 40 45  
 Ser Ala Asp Ala His Glu Lys Glu Phe Arg Ala Leu Glu Lys Lys Phe

50					55					60					
Asp	Ala	His	Pro	Gly	Val	Tyr	Ala	Ile	Asp	Thr	Arg	Asp	Gly	Gln	Glu
65					70					75					80
Ile	Thr	His	Arg	Ala	Asp	Glu	Arg	Phe	Ala	Tyr	Gly	Ser	Thr	Phe	Lys
				85					90					95	
Ala	Leu	Gln	Ala	Gly	Ala	Ile	Leu	Ala	Gln	Val	Leu	Arg	Asp	Gly	Arg
			100					105					110		
Glu	Val	Arg	Arg	Gly	Ala	Glu	Ala	Asp	Gly	Met	Asp	Lys	Val	Val	His
		115					120					125			
Tyr	Gly	Gln	Asp	Ala	Ile	Leu	Pro	Asn	Ser	Pro	Val	Thr	Glu	Lys	His
	130					135					140				
Val	Ala	Asp	Gly	Met	Ser	Leu	Arg	Glu	Leu	Cys	Asp	Ala	Val	Val	Ala
145					150					155					160
Tyr	Ser	Asp	Asn	Thr	Ala	Ala	Asn	Leu	Leu	Phe	Asp	Gln	Leu	Gly	Gly
				165					170					175	
Arg	Arg	Gly	Ser	Thr	Arg	Val	Leu	Lys	Gln	Leu	Gly	Asp	His	Thr	Thr
			180					185					190		
Ser	Met	Asp	Arg	Tyr	Glu	Gln	Glu	Leu	Gly	Ser	Ala	Val	Pro	Gly	Asp
		195					200					205			
Pro	Arg	Asp	Thr	Ser	Thr	Pro	Arg	Ala	Phe	Ala	Glu	Asp	Leu	Arg	Ala
		210				215					220				
Phe	Ala	Val	Glu	Asp	Gly	Glu	Lys	Ala	Ala	Leu	Ala	Pro	Asn	Asp	Arg
225					230					235					240
Glu	Gln	Leu	Asn	Asp	Trp	Met	Ser	Gly	Ser	Arg	Thr	Gly	Asp	Ala	Leu
				245					250					255	
Ile	Arg	Ala	Gly	Val	Pro	Lys	Asp	Trp	Lys	Val	Glu	Asp	Lys	Ser	Gly
			260					265					270		
Gln	Val	Lys	Tyr	Gly	Thr	Arg	Asn	Asp	Ile	Ala	Val	Val	Arg	Pro	Pro
		275					280					285			
Gly	Arg	Ala	Pro	Ile	Val	Val	Ser	Val	Met	Ser	His	Gly	Asp	Thr	Gln
		290				295					300				
Asp	Ala	Glu	Pro	His	Asp	Glu	Leu	Val	Ala	Glu	Ala	Gly	Leu	Val	Val
305					310					315					320
Ala	Asp	Gly	Leu	Lys											
				325											

&lt;210&gt; 7

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;400&gt; 7

tcagttaaca atttcaacaa agaacaacaa aatgct

36

<210> 8  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 8  
tcgaaatddd ttgttgtctt cctcttttgg

30

<210> 9  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 9  
catatgaaaa agaaaaacat ttattcaatt cgt

33

<210> 10  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 10  
ggatccttat agttcgcgac gacgtccagc taa

33

<210> 11  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 11  
cgggagctca ggctcaccca gaaacgctgg tg

32

<210> 12  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 12  
cgggaattct caccaatgct taatcagtga ggcacc

36

<210> 13  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 13  
ggctgtactt acaaattaat ccttaatggt aaaacattg

39

<210> 14  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 14  
ctctctttca gttaccgtaa aggtcttagt cgc

33

<210> 15  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 15  
aggttttatc catacgacgt cccggactac gccacaact

39

<210> 16  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 16  
agttgtggcg tagtccggga cgtcgtatgg ataaaacct

39

<210> 17  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 17  
ctcgagaaaa gaaatttggt gaatttccac

30

<210> 18  
<211> 30  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 18

gcaacgtgga gtgctccctc tgcagtgttt

30

<210> 19

<211> 90

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 19

ccgatcatca aactttctcaa gctgcttaaa ctccctgcgcc ggaaacttct caagctgctt 60  
aaactcctgc cggatcagga gtttaagcag 90

<210> 20

<211> 90

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 20

ctgcttaaac tcttgatccg gcaggagttt aagcagcttg agaagtttcc ggcgcaggag 60  
tttaagcagc ttgagaagtt tgatgatcgg 90

<210> 21

<211> 54

<212> DNA

<213> Escherichia coli

<220>

<223> STa, heat-stable enterotoxin

<400> 21

aacacgtttt actgctgcga actttgctgc aaccacagcat gcgcaggttg ctac 54

<210> 22

<211> 18

<212> PRT

<213> Escherichia coli

<220>

<223> STa, heat-stable enterotoxin

<400> 22

Asn Thr Phe Tyr Cys Cys Glu Leu Cys Cys Asn Pro Ala Cys Ala Gly  
1 5 10 15

Cys Tyr



<210> 23  
<211> 201  
<212> DNA  
<213> Staphylococcus aureus

<220>  
<223> Protein A, one Fc binding domain

<400> 23  
tcagtgaaca atttcaacaa agaacaacaa aatgctttct atgaaatttt acattttacct 60  
aacttaactg aagaacaacg taacggcttc atccaaagcc ttaaagacga tccttcagtg 120  
agcaaagaaa ttttagcaga agctaaaaag ctaaacgatg ctcaagcacc aaaagaggaa 180  
gacaacaaga aaaaatttcg a 201

<210> 24  
<211> 67  
<212> PRT  
<213> Staphylococcus aureus

<220>  
<223> Protein A, one Fc binding domain

<400> 24  
Ser Val Asn Asn Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile  
1 5 10 15  
Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln  
20 25 30  
Ser Leu Lys Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala  
35 40 45  
Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Glu Glu Asp Asn Lys Lys  
50 55 60  
Lys Phe Arg  
65

<210> 25  
<211> 375  
<212> DNA  
<213> Staphylococcus aureus

<220>  
<223> Protein A, two Fc binding domains

<400> 25  
tcagtgaaca atttcaacaa agaacaacaa aatgctttct atgaaatctt gaacatgcct 60  
aacttgaacg aagaacaacg caatgggttc atccaaagct taaaagatga cccaagtcaa 120  
agtgcatacc ttttagcaga agctaaaaag ttaaataaat ctcaagcacc gaaagctgat 180  
aacaatttca acaaagaaca acaaaatgct ttctatgaaa ttttacattt acctaactta 240  
actgaagaac aacgtaacgg cttcatccaa agccttaaag acgatccttc agtgagcaaa 300  
gaaatttttag cagaagctaa aaagctaaac gatgctcaag caccaaaaga ggaagacaac 360  
aagaaaaaat ttcga 375

<210> 26  
<211> 125  
<212> PRT  
<213> Staphylococcus aureus

&lt;220&gt;

&lt;223&gt; Protein A, two Fc binding domains

&lt;400&gt; 26

Ser Val Asn Asn Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile  
 1 5 10 15

Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln  
 20 25 30

Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala  
 35 40 45

Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn  
 50 55 60

Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu  
 65 70 75 80

Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro  
 85 90 95

Ser Val Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala  
 100 105 110

Gln Ala Pro Lys Glu Glu Asp Asn Lys Lys Lys Phe Arg  
 115 120 125

&lt;210&gt; 27

&lt;211&gt; 177

&lt;212&gt; DNA

&lt;213&gt; Streptococcus pyogenes

&lt;220&gt;

&lt;223&gt; Protein G, one Fc binding domain

&lt;400&gt; 27

ggctgtactt acaaattaat ccttaatggt aaaacattga aaggccaaac aactactgaa 60  
 gctgttgatg ctgctactgc agaaaaagtc ttcaaacaat acgctaacga caacgggtgtt 120  
 gacgggtgaat ggacttacga cgatgcgact aagaccttta cggtactga aagagaa 177

&lt;210&gt; 28

&lt;211&gt; 59

&lt;212&gt; PRT

&lt;213&gt; Streptococcus pyogenes

&lt;220&gt;

&lt;223&gt; Protein G, one Fc binding domain

&lt;400&gt; 28

Gly Cys Thr Tyr Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys Gly Gln  
 1 5 10 15

Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val Phe Lys  
 20 25 30

Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp Asp  
 35 40 45

Ala Thr Lys Thr Phe Thr Val Thr Glu Arg Glu  
 50 55

<210> 29  
 <211> 387  
 <212> DNA  
 <213> Streptococcus pyogenes

<220>  
 <223> Protein G, two Fc binding domains

<400> 29  
 ggctgtactt acaaattaat ccttaatggt aaaacattga aaggccaaac aactactgaa 60  
 gctgttgatg ctgctactgc agaaaaagtc ttcaaacaat acgctaacga caacgggtgtt 120  
 gacgggtgaat ggacttacga cgatgcgact aagaccttta cagttactga aaaaccagaa 180  
 gtgatcgatg cgtctgaatt aacaccagcc gtgacaactt acaaacttgt tattaatggt 240  
 aaaacattga aaggcgaaac aactactaaa gcagtagacg cagaaactgc agaaaaagcc 300  
 ttcaaacaat acgctaacga caacgggtgtt gatgggtgtt ggacttatga tgatgcgact 360  
 aagaccttta cggtactga aagagag 387

<210> 30  
 <211> 129  
 <212> PRT  
 <213> Streptococcus pyogenes

<220>  
 <223> Protein G, two Fc binding domains

<400> 30  
 Gly Cys Thr Tyr Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys Gly Gln  
     1                    5                    10                    15  
 Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val Phe Lys  
             20                    25                    30  
 Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp Asp  
             35                    40                    45  
 Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile Asp Ala  
             50                    55                    60  
 Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile Asn Gly  
     65                    70                    75                    80  
 Lys Thr Leu Lys Gly Glu Thr Thr Thr Lys Ala Val Asp Ala Glu Thr  
             85                    90                    95  
 Ala Glu Lys Ala Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly  
             100                    105                    110  
 Val Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Arg  
             115                    120                    125  
 Glu

<210> 31  
 <211> 39  
 <212> DNA  
 <213> Influenza virus

<220>

<223> hemagglutinin epitope

<400> 31

agggttttatc catacgacgt cccggactac gccacaact

39

<210> 32

<211> 13

<212> PRT

<213> Influenza virus

<220>

<223> Hemagglutinin epitope

<400> 32

Arg Phe Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Thr Thr

1

5

10

<210> 33

<211> 384

<212> DNA

<213> Homo sapiens

<220>

<223> phospholipase (hPLA2)

<400> 33

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ctcgagaaaa gaaatttggt gaatttccac agaattgatca agttgacgac aggaaaggaa 60
gccgcactca gttatggctt ctacggctgc cactgtggcg tgggtggcag aggatccccc 120
aaggatgcaa cggatcgctg ctgtgtcact catgactgtt gctacaaacg tctggagaaa 180
cgtggatgtg gcaccaaatt tctgagctac aagtttagca actcggggag cagaatcacc 240
tgtgcaaaac aggactcctg cagaagtcaa ctgtgtgagt gtgataaggc tgctgccacc 300
tgttttgcta gaaacaagac gacctacaat aaaaagtacc agtactattc caataaacac 360
tgcagaggga gcactccacg ttgc                                     384
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<210> 34

<211> 128

<212> PRT

<213> Homo sapiens

<220>

<223> phospholipase (hPLA2)

<400> 34

Leu Glu Lys Arg Asn Leu Val Asn Phe His Arg Met Ile Lys Leu Thr

1

5

10

15

Thr Gly Lys Glu Ala Ala Leu Ser Tyr Gly Phe Tyr Gly Cys His Cys

20

25

30

Gly Val Gly Gly Arg Gly Ser Pro Lys Asp Ala Thr Asp Arg Cys Cys

35

40

45

Val Thr His Asp Cys Cys Tyr Lys Arg Leu Glu Lys Arg Gly Cys Gly

50

55

60

Thr Lys Phe Leu Ser Tyr Lys Phe Ser Asn Ser Gly Ser Arg Ile Thr

65

70

75

80

Cys Ala Lys Gln Asp Ser Cys Arg Ser Gln Leu Cys Glu Cys Asp Lys

85

90

95

Ala Ala Ala Thr Cys Phe Ala Arg Asn Lys Thr Thr Tyr Asn Lys Lys  
                   100                  105                  110

Tyr Gln Tyr Tyr Ser Asn Lys His Cys Arg Gly Ser Thr Pro Arg Cys  
           115                  120                  125

<210> 35  
 <211> 90  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: affinity to  
       LPS

<400> 35  
 ccgatcatca aacttctcaa gctgcttaaa ctcctgcgcc ggaaacttct caagctgctt 60  
 aaactcctgc cggatcagga gttaagcag                                  90

<210> 36  
 <211> 30  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: affinity to  
       LPS

<400> 36  
 Pro Ile Ile Lys Leu Leu Lys Leu Leu Lys Leu Leu Arg Arg Lys Leu  
   1                  5                  10                  15  
 Leu Lys Leu Leu Lys Leu Leu Pro Asp Gln Glu Phe Lys Gln  
                   20                  25                  30

<210> 37  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> HA peptide containing linker

<220>  
 <223> Description of Artificial Sequence: peptide

<400> 37  
 Gly Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Gly  
   1                  5                  10                  15

<210> 38  
 <211> 377  
 <212> PRT

&lt;213&gt; Escherichia coli

&lt;220&gt;

<223> AmpC  $\beta$ -lactamase Protein

&lt;400&gt; 38

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Met Phe Lys Thr Thr Leu Cys Ala Leu Leu Ile Thr Ala Ser Cys Ser
 1              5              10              15

Thr Phe Ala Ala Pro Gln Gln Ile Asn Asp Ile Val His Arg Thr Ile
      20              25              30

Thr Pro Leu Ile Glu Gln Gln Lys Ile Pro Gly Met Ala Val Ala Val
      35              40              45

Ile Tyr Gln Gly Lys Pro Tyr Tyr Phe Thr Trp Gly Tyr Ala Asp Ile
      50              55              60

Ala Lys Lys Gln Pro Val Thr Gln Gln Thr Leu Phe Glu Leu Gly Ser
      65              70              75              80

Val Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp Ala Ile Ala Arg
      85              90              95

Gly Glu Ile Lys Leu Ser Asp Pro Thr Thr Lys Tyr Trp Pro Glu Leu
      100              105              110

Thr Ala Lys Gln Trp Asn Gly Ile Thr Leu Leu His Leu Ala Thr Tyr
      115              120              125

Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu Val Lys Ser Ser
      130              135              140

Ser Asp Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro Ala Trp Ala Pro
      145              150              155              160

Gly Thr Gln Arg Leu Tyr Ala Asn Ser Ser Ile Gly Leu Phe Gly Ala
      165              170              175

Leu Ala Val Lys Pro Ser Gly Leu Ser Phe Glu Gln Ala Met Gln Thr
      180              185              190

Arg Val Phe Gln Pro Leu Lys Leu Asn His Thr Trp Ile Asn Val Pro
      195              200              205

Pro Ala Glu Glu Lys Asn Tyr Ala Trp Gly Tyr Arg Glu Gly Lys Ala
      210              215              220

Val His Val Ser Pro Gly Ala Leu Asp Ala Glu Ala Tyr Gly Val Lys
      225              230              235              240

Ser Thr Ile Glu Asp Met Ala Arg Trp Val Gln Ser Asn Leu Lys Pro
      245              250              255

Leu Asp Ile Asn Glu Lys Thr Leu Gln Gln Gly Ile Gln Leu Ala Gln
      260              265              270

Ser Arg Tyr Trp Gln Thr Gly Asp Met Tyr Gln Gly Leu Gly Trp Glu
      275              280              285

Met Leu Asp Trp Pro Val Asn Pro Asp Ser Ile Ile Asn Gly Ser Asp
      290              295              300

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Asn Lys Ile Ala Leu Ala Ala Arg Pro Val Lys Ala Ile Thr Pro Pro  
 305 310 315 320  
 Thr Pro Ala Val Arg Ala Ser Trp Val His Lys Thr Gly Ala Thr Gly  
 325 330 335  
 Gly Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys Glu Leu Gly Ile  
 340 345 350  
 Val Met Leu Ala Asn Lys Asn Tyr Pro Asn Pro Ala Arg Val Asp Ala  
 355 360 365  
 Ala Trp Gln Ile Leu Asn Ala Leu Gln  
 370 375

<210> 39  
 <211> 1140  
 <212> DNA  
 <213> Escherichia coli

<220>  
 <223> AmpC  $\beta$ -lactamase gene

<400> 39  
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 atcccgggta tggcgggtggc ggtaatttat cagggtaaac cttattactt tacctggggc 180  
 tatgcggaaca tcgcaaaaaa gcagcccgctc acacagcaaa cgttggttga gttaggttcg 240  
 gtcagcaaaa catttactgg cgtgcttggt ggcgacgcta ttgctcgagg ggaaatcaag 300  
 ttaagcgatc ccacaacaaa atactggcct gaacttaccg ctaaacagtg gaatgggatc 360  
 acactattac atctcgcaac ctacactgct ggcggcctgc cattgcaggt gccggatgag 420  
 gtgaaatcct caagcgactt gctgcgcttc tatcaaaact ggcagcctgc atgggctcca 480  
 ggaacacaac gtctgtatgc caactccagt atcggtttgt tcggcgcaact ggctgtgaag 540  
 ccgtctggtt tgagttttga gcaggcgatg caaactcgtg tcttccagcc actcaaactc 600  
 aaccatacgt ggattaatgt accgcccga gaagaaaaga attacgcctg gggatatcgc 660  
 gaaggtaagg cagtgcattg ttcgcctggg gcgttagatg ctgaagctta tgggtgtgaag 720  
 tcgaccattg aagatatggc ccgctgggtg caaagcaatt taaaaccctc tagtactgat 780  
 atcaatgaga aaacgcttca acaagggata caactggcac aatctcgcta ctggcaaacc 840  
 ggcgatatgt atcagggcct gggctgggaa atgctggact ggccggtaaa tcctgacagc 900  
 atcattaacg gcagtgcaca taaaattgca ctggcagcac gccccgtaaa agcgattacg 960  
 cccccaactc ctgcagtacg cgcacatcatg gtacataaaa caggggacgc cggcggtatt 1020  
 ggtagctatg tcgcgtttat tccagaaaaa gagctgggta tcgtgatgct ggcaacaaaa 1080  
 aactatccca atccagcgag agtcgacgac gcctggcaga ttcttaacgc tctacagtaa 1140

<210> 40  
 <211> 256  
 <212> PRT  
 <213> Bacillus licheniformis

<220>  
 <223> BlaR-CTD  $\beta$ -lactamase

<400> 40  
 Met Gln Lys Glu Thr Arg Phe Leu Pro Gly Thr Asn Val Glu Tyr Glu  
 1 5 10 15  
 Asp Tyr Ser Thr Phe Phe Asp Lys Phe Ser Ala Ser Gly Gly Phe Val  
 20 25 30  
 Leu Phe Asn Ser Asn Arg Lys Lys Tyr Thr Ile Tyr Asn Arg Lys Glu

35	40	45
Ser Thr Ser Arg Phe Ala Pro Ala Ser Thr Tyr Lys Val Phe Ser Ala		
50	55	60
Leu Leu Ala Leu Glu Ser Gly Ile Ile Thr Lys Asn Asp Ser His Met		
65	70	75
Thr Trp Asp Gly Thr Gln Tyr Pro Tyr Lys Glu Trp Asn Gln Asp Gln		
85	90	95
Asp Leu Phe Ser Ala Met Ser Ser Ser Thr Thr Trp Tyr Phe Gln Lys		
100	105	110
Leu Asp Arg Gln Ile Gly Glu Asp His Leu Arg His Tyr Leu Lys Ser		
115	120	125
Ile His Tyr Gly Asn Glu Asp Phe Ser Val Pro Ala Asp Tyr Trp Leu		
130	135	140
Asp Gly Ser Leu Gln Ile Ser Pro Leu Glu Gln Val Asn Ile Leu Lys		
145	150	155
Lys Phe Tyr Asp Asn Glu Phe Asp Phe Lys Gln Ser Asn Ile Glu Thr		
165	170	175
Val Lys Asp Ser Ile Arg Leu Glu Glu Ser Asn Gly Arg Val Leu Ser		
180	185	190
Gly Lys Thr Gly Thr Ser Val Ile Asn Gly Glu Leu His Ala Gly Trp		
195	200	205
Phe Ile Gly Tyr Val Glu Thr Ala Asp Asn Thr Phe Phe Phe Ala Val		
210	215	220
His Ile Gln Gly Glu Lys Arg Ala Ala Gly Ser Ser Ala Ala Glu Ile		
225	230	235
Ala Leu Ser Ile Leu Asp Lys Lys Gly Ile Tyr Pro Ser Val Ser Arg		
245	250	255

&lt;210&gt; 41

&lt;211&gt; 768

&lt;212&gt; DNA

&lt;213&gt; Bacillus licheniformis

&lt;220&gt;

<223> BlaR-CTD  $\beta$ -lactamase gene

&lt;400&gt; 41

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atgcaaaaag aaacacgctt tttacccggc accaatgtag aatacgaaga ttacagcact 60
ttttttgata aattttcagc ctcagggggc tttgtcctgt ttaattctaa taggaaaaag 120
tatacaatat acaataggaa agaaagcacc tccagattcg cacctgcttc cacctacaag 180
gtgttttagcg cattgctcgc actggaatcc gggatcatca cgaagaacga ctctcacatg 240
acttgggatg ggaactcaata tccgtataaa gaatggaatc aagaccagga tttatttctt 300
gcgatgagca gctccacaac atggtatttt caaaaattgg accggcaa at tggggaggat 360
catttacgctc attatctcaa atctatacat tatggaaatg aggatttttc agtcccggcc 420
gattattggc tggatggctc tcttcaaatt tctccacttg aacaggtcaa tatattaaaa 480
aagttttatg ataacgaatt tgatttttaa cagtctaata ttgaaactgt gaaagattcg 540
atacgtttag aagaatcaaa tggcagggtt ttatccggtg aaaccggaac ctcggtaatc 600

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aacggggaac tccatgccgg ttggtttata gggatatgtag aaactgccga taatactttt 660
ttctttgctg ttcattttca aggtgaaaaa cgggctgccg gaagctccgc tgccgaaatt 720
gcactttcca ttttagataa aaaagggtatt tatccctccg tttcccga 768
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